

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Genencor International, Inc.
- (ii) TITLE OF THE INVENTION: ESTERASE ENZYMES, DNA ENCODING
ESTERASE ENZYMES AND VECTORS AND HOST CELLS INCORPORATING SAME
- (iii) NUMBER OF SEQUENCES: 35
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Genencor International, Inc.
(B) STREET: 925 Page Mill Road
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304-1013
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/952,445
(B) FILING DATE: 18-NOV-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/722,713
(B) FILING DATE: 30-SEP-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Stone, Christopher L.
(B) REGISTRATION NUMBER: 35,696
(C) REFERENCE/DOCKET NUMBER: GC362-2-US
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650-846-7555
(B) TELEFAX: 650-845-6504

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala Ser Thr Gln Gly Ile Ser Glu Asp Leu Tyr Ser Arg Leu Val Glu
1 5 10 15

Met Ala Thr Ile Ser Gln Ala Ala Tyr Xaa Asp Leu Leu Asn Ile Pro
20 25 30

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa Thr Val Gly Phe Gly Pro Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Phe Gly Leu His Leu Xaa Gln Xaa Met
1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Xaa Ile Ser Glu Asp Leu Tyr Ser
1 5

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Tyr Ile Gly Trp Ser Phe Tyr Asn Ala
1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gly Ile Ser Glu Asp Leu Tyr Xaa Xaa Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Xaa Ile Ser Glu Ser Leu Tyr Xaa Xaa Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Gly Ile Ser Glu Asp Leu Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Leu Glu Pro Pro Tyr Thr Gly
1 5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Xaa Ala Asn Asp Gly Ile Pro Asn Leu Pro Pro Val Glu Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Tyr Pro Asp Tyr Ala Leu Tyr Lys
1 5

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGGGAATTCG CWSACCARGG AT

22

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ala	Ser	Thr	Gln	Gly	Ile	Ser	Glu	Asp	Leu	Tyr	Ser	Arg	Leu	Val	Glu
1				5					10					15	
Met	Ala	Thr	Ile	Ser	Gln	Ala	Ala	Tyr	Ala	Asp	Leu	Leu	Asn	Ile	Pro
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGGGAATTCT AYTAYATHGG TGGGT

25

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Val	His	Gly	Gly	Tyr	Tyr	Ile	Gly	Trp	Val	Ser	Val	Gln	Asp	Gln	Val
1				5				10						15	

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGGGAATTCA CCCACCDATR TARTA

25

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Val His Gly Gly Tyr Tyr Ile Gly Trp Val Ser Val Gln Asp Gln Val

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGGGAATTCT TGGATCCRTC RTT

23

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Thr	Asp	Ala	Phe	Gln	Ala	Ser	Ser	Pro	Asp	Thr	Thr	Gln	Tyr	Phe	Arg
1				5				10						15	
Val	Thr	His	Ala	Asn	Asp	Gly	Ile	Pro	Asn	Leu					
			20					25							

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CGGGAATTCA TCCRTCRTTG CRTG

24

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Thr Asp Ala Phe Gln Ala Ser Ser Pro Asp Thr Thr Gln Tyr Phe Arg

1	5	10	15
Val	Thr	His	Ala
	Asn	Asp	Gly
	Ile	Pro	Asn
	Leu		
20	25		

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGGGAATTCG CYTGRAAGCR TCGTCAT

27

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Thr	Asp	Ala	Phe	Gln	Ala	Ser	Ser	Pro	Asp	Thr	Thr	Gln	Tyr	Phe
1				5					10					15	
Arg	Val	Thr	His	Ala	Asn	Asp	Gly	Ile	Pro	Asn	Leu				
			20					25							

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met	Thr	Asp	Ala	Phe	Gln	Ala	Ser	Ser	Pro	Asp	Thr	Thr	Gln	Tyr	Phe
1				5					10					15	
Arg	Val	Thr	His	Ala	Asn	Asp	Gly	Ile	Pro	Asn	Leu				
			20					25							

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 650 base pairs
- (B) TYPE: nucleic acid

(D) TOPOLOGY: linear

GCCTCTACGC	AGGGCATCTC	CGAAGACCTC	TACAGCCGTT	TAGTCGAAAT	GGCCACTATC	60
TCCCAAGCTG	CCTACGCCGA	CCTGTGCAAC	ATTCCGTCGA	CTATTATCAA	GGGAGAGAAA	120
ATTTACAATT	CTCAAACCTGA	CATTAACGGA	TGGATCCTCC	GCGACGACAG	CAGCAAAGAA	180
ATAATCACCG	TCTTCCGTGG	CACTGGTAGT	GATACGAATC	TACAACTCGA	TACTAACTAC	240
ACCCTCACGC	CTTTCGACAC	CCTACCACAA	TGCAACGGTT	GTGAAGTACA	CGGTGGATAT	300
TATATTGGAT	GGGTCTCCGT	CCAGGACCAA	GTCGAGTCGC	TTGTCAAACA	GCAGGTTAGC	360
CAGTATCCGG	ACTATGCGCT	GACTGTGACG	GGCCACAGGT	ATGCCCTCGT	GATTTCTTTC	420
AATTAAGTGT	ATAATACTCA	CTAACTCTAC	GATAGTCTCG	GAGCGTCCCT	GGCAGCACTC	480
ACTGCCGCC	AGCTGTCTGC	GACATACGAC	AACATCCGCC	TGTACACCTT	CGGCGAACCG	540
CGCAGCGGCA	ATCAGGCCCTT	CGCGTCGTAC	ATGAACGATG	CCTTCCAAGC	CTCGAGCCCA	600
GATACGACGC	AGTATTTCCG	GGTCACTCAT	GCCAACGACG	GCATCCCAA		650

(D) TOPOLOGY: linear

[illegible]

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCATGGTGGT	GTCGATATCG	GCAGTAGTCT	TTGCCGAAAC	GTTGAGGGTT	ACAGTGATCT	60
GCGTCGGACA	TACTTCGGGG	AATCTACGGC	GGAATATCAA	AGTCTTCGGA	ATATCCATAT	120
TGGGAAAGGA	CAGAAGCTCC	GGGGTAGTTT	GATAGATGAG	CTCCGGTGTA	TTAAATCGGG	180
AGCTGACAGG	AGTGAGCGTC	ATGTAGACCA	TCTAGTAATG	TCAGTCGCGC	GCAATTTTCGC	240
ACATGAAACA	AGTTGATTTT	GGGACCCCAT	TGTTACATCT	CTCGGCTACA	GCTCGAGATG	300
TGCCTGCCGA	GTATACTTAG	AAGCCATGCC	AGCGTGTTGT	TATACGACCA	AAAGTCAGGG	360
AATATGAAAC	GATCGTCGGA	TATTTCTTGT	TTTTATCCTA	AATTAGTCTT	CCAGTGGTTT	420
ATTTAAGAGA	TAGATCCCTT	CACAAACACT	CATCCAACGG	ACTTCTCATA	CCACTCATTG	480
ACATAATTTT	AAACAGCTCC	AGGCGCATTT	AGTTCAACAT	GAAGCAATTC	TCCGCCAAAC	540
ACGTCTCTCG	AGTTGTGGTG	ACTGCAGGGC	ACGCTTAGC	AGCCTCTACG	CAAGGCATCT	600
CCGAAGACCT	CTACAGCCGT	TTAGTCGAAA	TGGCCACTAT	CTCCAAGCT	GCCTACGCCG	660
ACCTGTGCAA	CATTCCGTCG	ACTATTATCA	AGGGAGAGAA	AATTTACAAT	TCTCAAACCTG	720
ACATTAACGG	ATGGATCCTC	CGCGACGACA	GCAGCAAAGA	AATAATCACC	GTCTTCCGTG	780
GCACTGGTAG	TGATACGAAT	CTACAACCTG	ATACTAACTA	CACCCTCACG	CCTTTCGACA	840
CCCTACCACA	ATGCAACGGT	TGTGAAGTAC	ACGGTGGATA	TTATATTGGA	TGGGTCTCCG	900
TCCAGGACCA	AGTCGAGTCG	CTTGTCAAAC	AGCAGGTTAG	CCAGTATCCG	GACTATGCGC	960
TGACTGTGAC	GGGCCACAGG	TATGCCCTCG	TGATTTCTTT	CAATTAAGTG	TATAATACTC	1020
ACTAACTCTA	CGATAGTCTC	GGAGCGTCCC	TGGCAGCACT	CACTGCCGCC	CAGCTGTCTG	1080
CGACATACGA	CAACATCCGC	CTGTACACCT	TCGGCGAACC	GCGCAGCGGC	AATCAGGCCT	1140
TCGCGTCGTA	CATGAACGAT	GCCTTCCAAG	CCTCGAGCCC	AGATACGACG	CAGTATTTCC	1200
GGGTCACTCA	TGCCAACGAC	GGCATCCCAA	ACCTGCCCCC	GGTGGAGCAG	GGGTACGCCC	1260
ATGGCGGTGT	AGAGTACTGG	AGCGTTGATC	CTTACAGCGC	CCAGAACACA	TTTGTCTGCA	1320
CTGGGGATGA	AGTGCAGTGC	TGTGAGGCCC	AGGGCGGACA	GGGTGTGAAT	AATGCGCACA	1380
CGACTTATTT	TGGGATGACG	AGCGGAGCCT	GTACATGGTG	ATCAGTCATT	TCAGCCTCCC	1440
CGAGTGTACC	AGGAAAGATG	GATGTCCTGG	AGAGGGCATG	CATGTACGTA	TACCCGAAGC	1500
ACACTTTTTT	GGTAAATCAG	GACATGTAAT	AAGTTCCTTC	CATGAATAGA	TATGGTTACC	1560
CTCACCATAA	GCCTTGAGGT	TGCCTTTCTC	TTTTGATTGT	GAATATATAT	TTAAAGTAGA	1620
TGACAGATAT	CTCTAAACAC	CTTATCCGCT	TAAACCCATC	ATAGATTGTG	TCACGTGATA	1680
GACCCCTTGA	ATGATGAGCG	AAATGTATCA	GTCCCGTTTA	AATCAAACCC	TTTCAGCCTA	1740
GCACAGTCAG	AATACACCAA	CCCATTCTA	AGGTAGTACT	AAATATGAAT	ACAGCCTAAA	1800
TGCATCGCTA	TATGATCCCA	TAAAGAAGCA	ACAACCTTTC	AGATCTCGTT	TTGCGCTGCG	1860
AAGAGCTAGC	TCTACCATGG	TCTCAATTAT	GAGTGGAGCG	TTTAGTCTCG	TTTAAGCCTA	1920
GCTATCTTAT	AAGGACAACA	CATGTACATG	GGCTTACTTG	TAGAGAGGTA	GGATCCCCGG	1980
CTTCTTCACA	TCTCGAGGAG	TTGTCTACAC	GTCGCGTCCA	TGTCATAAGC	CGGTACTCGA	2040
CGTTGTCTGT	ACCGTGACCC	AGACCCCTGT	TGATAGCGTT	GAGAAGGCCC	TATATTTGAA	2100
TTTCCAATCT	CAGCTTTACG	AAGATATGCC	CATGGTGGAG	GGTTAGTAAA	CCGATGATGA	2160
TCGTGTGCAG	CATGAGATGA	GACCGTGGCC	AATCCTGTTC	AAATGCCAAG	ACCCGCTTCC	2220
TACCACATGT	AAGGCATCCG	TCGGCCGCAC	GTTGAATTGT	GCAAATGCCG	AGATCATAAA	2280
AGCGGCCACA	CTTCCACGTC	GGTACTGGAT	GGGTTGCGCG	TGGCCATACT	GTGTTTTCCA	2340
TTGCGTGGGT	CGTTCGTGTT	ACTGCGACGC	AGATTCTGTA	GGCAAGGCGC	AGGGCTCTCT	2400
TCTGAGGTAG	AAAACACCCC	ATATTAATCT	GAATTC			2436

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 281 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met	Lys	Gln	Phe	Ser	Ala	Lys	His	Val	Leu	Ala	Val	Val	Val	Thr	Ala
1				5					10					15	
Gly	His	Ala	Leu	Ala	Ala	Ser	Thr	Gln	Gly	Ile	Ser	Glu	Asp	Leu	Tyr
			20					25					30		
Ser	Arg	Leu	Val	Glu	Met	Ala	Thr	Ile	Ser	Gln	Ala	Ala	Tyr	Ala	Asp
			35				40					45			
Leu	Cys	Asn	Ile	Pro	Ser	Thr	Ile	Ile	Lys	Gly	Glu	Lys	Ile	Tyr	Asn
			50			55					60				
Ser	Gln	Thr	Asp	Ile	Asn	Gly	Trp	Ile	Leu	Arg	Asp	Asp	Ser	Ser	Lys
65					70				75						80
Glu	Ile	Ile	Thr	Val	Phe	Arg	Gly	Thr	Gly	Ser	Asp	Thr	Asn	Leu	Gln
				85					90					95	
Leu	Asp	Thr	Asn	Tyr	Thr	Leu	Thr	Pro	Phe	Asp	Thr	Leu	Pro	Gln	Cys
			100					105					110		
Asn	Gly	Cys	Glu	Val	His	Gly	Gly	Tyr	Tyr	Ile	Gly	Trp	Val	Ser	Val
			115				120					125			
Gln	Asp	Gln	Val	Glu	Ser	Leu	Val	Lys	Gln	Gln	Val	Ser	Gln	Tyr	Pro
			130				135				140				
Asp	Tyr	Ala	Leu	Thr	Val	Thr	Gly	His	Ser	Leu	Gly	Ala	Ser	Leu	Ala
145					150				155						160
Ala	Leu	Thr	Ala	Ala	Gln	Leu	Ser	Ala	Thr	Tyr	Asp	Asn	Ile	Arg	Leu
				165					170					175	
Tyr	Thr	Phe	Gly	Glu	Pro	Arg	Ser	Gly	Asn	Gln	Ala	Phe	Ala	Ser	Tyr
			180					185					190		
Met	Asn	Asp	Ala	Phe	Gln	Ala	Ser	Ser	Pro	Asp	Thr	Thr	Gln	Tyr	Phe
			195				200					205			
Arg	Val	Thr	His	Ala	Asn	Asp	Gly	Ile	Pro	Asn	Leu	Pro	Pro	Val	Glu
			210				215				220				
Gln	Gly	Tyr	Ala	His	Gly	Gly	Val	Glu	Tyr	Trp	Ser	Val	Asp	Pro	Tyr
225					230					235					240
Ser	Ala	Gln	Asn	Thr	Phe	Val	Cys	Thr	Gly	Asp	Glu	Val	Gln	Cys	Cys
				245					250					255	
Glu	Ala	Gln	Gly	Gly	Gln	Gly	Val	Asn	Asn	Ala	His	Thr	Thr	Tyr	Phe
			260					265					270		
Gly	Met	Thr	Ser	Gly	Ala	Cys	Thr	Trp							
			275					280							

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2436 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CGCGCTGCAG GCTCTTTCTG GTAATACTAT GCTGG

35

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GGCTTAATTA ACGTGCTGGT CTCGGATCTT TGGCGG

36

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGGGCGCGCC AGATCTAGTA CCGATGTTGA GGATGAAGCT

40

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCCCAGATCT CCGCAATGAA GCAATTCTCC GCCAAACAC

39

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AATAGTCGAC GGAATGTTGC ACAGG
-- 27 --
GC362-2-PCT

25

GC362-2-PCT